

# Sequence Listing

<110> Baker, Kevin  
 Botstein, David  
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 Ferrara, Napoleone  
 Filvaroff, Ellen  
 Gerritsen, Mary  
 Goddard, Audrey  
 Godowski, Paul  
 Grimaldi, Christopher  
 Gurney, Austin  
 Hillan, Kenneth  
 Kljavin, Ivar  
 Napier, Mary  
 Roy, Margaret  
 Tumas, Daniel  
 Wood, William

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 10-23-97

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Pro	Arg	Ser	His	Phe	Phe	Pro	Phe	Asp	Leu	Phe	Pro	Met	Cys	Pro	
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Phe	Gly	Cys	Gln	Cys	Tyr	Ser	Arg	Val	Val	His	Cys	Ser	Asp	Leu	
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Leu	Asp	Leu	Gln	Asn	Asn	Lys	Ile	Lys	Glu	Ile	Lys	Glu	Asn	Asp	
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Phe	Lys	Gly	Leu	Thr	Ser	Leu	Tyr	Gly	Leu	Ile	Leu	Asn	Asn	Asn	
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Leu	Asn	Leu	Pro	Lys	Ser	Leu	Ala	Glu	Leu	Arg	Ile	His	Glu	Asn	
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Ile	Phe	Leu	His	Ser	Asn	Ser	Ile	Ala	Arg	Val	Gly	Val	Asn	Asp
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Ile	Ser	Leu	Phe	Asn	Asn	Pro	Val	Lys	Tyr	Trp	Glu	Met	Gln	Pro
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Arg Gly Ala Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu  
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Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met  
65 70 75

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Pro	Ser	Gly	Leu	Ser 140	Phe	Glu	Tyr	Pro	Arg 145	Asp	Pro	Glu	His	Arg 150
Ser	Tyr	Ser	Asp	Arg 155	Gly	Glu	Pro	Gly	Ala 160	Glu	Glu	Arg	Ala	Arg 165
Gly	Asp	Gly	His	Thr 170	Asp	Phe	Val	Ala	Leu 175	Leu	Thr	Gly	Pro	Arg 180
Ser	Gln	Ala	Val	Ala 185	Arg	Ala	Arg	Val	Ser 190	Leu	Leu	Arg	Ser	Ser 195
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Ile	Leu	Thr	Leu	Glu 290	Gly	Pro	Pro	Gln	Gln 295	Gly	Val	Gly	Gly	Ile 300
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Leu Arg Ile Ser Gly His Ile Ala Ala Arg Lys Ser Cys Asp Val	395	400	405
Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu Ile Pro Val Gln	410	415	420
Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu Gly Asn Gly	425	430	435
Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser Glu Val	440	445	450
Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln Arg	455	460	465
Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr	470	475	480
Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met	485	490	495
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Pro Asp Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys	515	520	525
Gly His Ser Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly	530	535	540
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Trp Leu Ser Leu Asp Thr His Cys His Leu His Tyr Glu Val Leu	560	565	570
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Gly Phe Tyr Gly Ser Glu Ala Gln Gly Val Val Lys Asp Leu Glu	605	610	615
Pro Glu Leu Leu Arg His Leu Ala Lys Gly Met Ala Ser Leu Met	620	625	630
Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu Leu Arg Gly Gln Val	635	640	645
His Ile Ala Asn Gln Cys Glu Val Gly Gly Leu Arg Leu Glu Ala	650	655	660

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Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys	695	700	705
Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro	710	715	720
Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr	725	730	735
Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His	740	745	750
Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys	755	760	765
Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro	770	775	780
Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala	785	790	795
Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys	800	805	810
Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys	815	820	825
Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg	830	835	840
Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly	845	850	855
Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg	860	865	870
Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp	875	880	885
His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys	890	895	900
Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser	905	910	915
Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser	920	925	930
Arg Cys Thr Ala His Arg Arg Pro Pro Glu Thr Arg Thr Asp Pro	935	940	945
Glu Leu Glu Lys Glu Ala Glu Gly Ser			

<210> 8  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide probe  
  
 <400> 8  
 gactagttct agatcgcgag cggccgccct tttttttttt tttt 44  
  
 <210> 9  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 9  
 cggacgcgtg gggcctgcgc acccagct 28  
  
 <210> 10  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 10  
 gccgctcccc gaacgggcag cggctccttc tcagaa 36  
  
 <210> 11  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 11  
 ggcgcacagc acgcagcgca tcaccccgaa tggctc 36  
  
 <210> 12  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic Oligonucleotide Probe  
  
 <400> 12  
 gtgctgccca tccgttctga gaagga 26  
  
 <210> 13

<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
gcaggggtgct caaacaggac ac 22

<210> 14  
<211> 3231  
<212> DNA  
<213> Homo Sapien

<400> 14  
ggcggagcag ccctagccgc caccgtcgtc ctgcagctc tcgtcgccac 50  
tgccaccgcc gccgccgtca ctgcgtcctg gtcgccgctc ccgcgccctc 100  
ccggccggcc atgcagcccc gccgcgcccga ggcgcccggt gcgcagctgc 150  
tgcccgcgct ggccctgctg ctgctgctgc tcggagcggg gccccgaggc 200  
agctccctgg ccaaccgggt gccgcgcgcg cccttgtctg cgcgccggcc 250  
gtgcgcgcgc cagccctgcc ggaatggggg tgtgtgcacc tcgcgccctg 300  
agccggaccc gcagcaccgc gccccgcgcg gcgagcctgg ctacagctgc 350  
acctgccccg ccgggatctc cggcgccaac tgccagcttg ttgcagatcc 400  
ttgtgccagc aacccttgct accatggcaa ctgcagcagc agcagcagca 450  
gcagcagcga tggctacctc tgcatttgca atgaaggcta tgaaggctcc 500  
aactgtgaac aggcaattcc cagtctccca gccactggct ggaccgaatc 550  
catggcaccg cgacagcttc agcctgttcc tgctactcag gagcctgaca 600  
aaatcctgcc tcgtctcag gcaacgggtga cactgcctac ctggcagccg 650  
aaaacagggc agaaagttgt agaaatgaaa tgggatcaag tggaggtgat 700  
cccagatatt gcctgtggga atgccagttc taacagctct gcgggtggcc 750  
gcctggtatc ctttgaagtg ccacagaaca cctcagtcaa gattcggcaa 800  
gatgccactg cctcactgat tttgctctgg aaggtcacgg ccacaggatt 850  
ccaacagtgc tccctcatag atggacgaag tgtgaccccc cttcaggctt 900  
cagggggact ggtcctcctg gaggagatgc tcgccttggg gaataatcac 950  
tttattggtt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000  
cttaactctg gtggtgaagg tcagcacctg tgtgccgggg gagagtcacg 1050

caaatgactt ggagtgttca ggaaaaggaa aatgcaccac gaagccgtca 1100  
 gaggcaactt tttcctgtac ctgtgaggag cagtacgtgg gtactttctg 1150  
 tgaagaatac gatgcttgcc agaggaaacc ttgccaaaac aacgcgagct 1200  
 gtattgatgc aaatgaaaag caagatggga gcaatttcac ctgtgtttgc 1250  
 cttcctgggt atactggaga gctttgccag tccaagattg attactgcat 1300  
 cctagacca tgcagaaatg gagcaacatg catttccagt ctgagtgat 1350  
 tcacctgcca gtgtccagaa ggatacttcg gatctgcttg tgaagaaaag 1400  
 gtggaccctt gcgcctcgtc tccgtgccag aacaacggca cctgctatgt 1450  
 ggacggggta cactttacct gcaactgcag cccgggcttc acagggccga 1500  
 cctgtgcccc gcttattgac ttctgtgccc tcagccctg tgctcatggc 1550  
 acgtgccga gcgtgggcac cagctacaaa tgctctgtg atccaggtta 1600  
 ccatggcctc tactgtgagg aggaatataa tgagtgcctc tccgctccat 1650  
 gctgaatgc agccacctgc agggacctcg ttaatggcta tgagtgtgtg 1700  
 tgctggcag aatacaaagg aacacactgt gaattgtaca aggatccctg 1750  
 cgtaacgtc agctgtctga acggagccac ctgtgacagc gacggcctga 1800  
 atggcacgtg catctgtgca cccgggttta caggtgaaga gtgcgacatt 1850  
 gacataaatg aatgtgacag taaccctcgc caccatgggt ggagctgcct 1900  
 ggaccagccc aatgggtata actgccactg cccgcatggt tgggtgggag 1950  
 caaactgtga gatccacctc caatggaagt cggggcacat ggcgagagc 2000  
 ctaccaaca tgccacggca ctccctctac atcatcattg gagccctctg 2050  
 cgtggccttc atccttatgc tgatcactc gatcgtgggg atttgccgca 2100  
 tcagccgcat tgaataccag ggttcttcca ggccagccta tgaggagtgc 2150  
 tacaactgcc gcagcatcga cagcgagtgc agcaatgcc ttgcatccat 2200  
 ccggcatgcc aggtttggaa agaaatcccg gcctgcaatg tatgatgtga 2250  
 gccccatgc ctatgaagat tacagtctc atgacaaacc cttggtcaca 2300  
 ctgattaaaa ctaaagattt gtaatctttt tttggattat ttttcaaaaa 2350  
 gatgagatac tacactcatt taaatatttt taagaaaata aaaagcttaa 2400  
 gaaattttaa atgctagctg ctcaagagtt ttcagtagaa tatttaagaa 2450  
 ctaattttct gcagctttta gtttgaaaaa aatattttta aaacaaaatt 2500

Year	Total population		Population aged 15 years and over		Population aged 65 years and over		Population aged 75 years and over	
	Number	Density	Number	Density	Number	Density	Number	Density
1980	1 000 000	100	700 000	70	100 000	10	20 000	2
1985	1 100 000	110	750 000	75	110 000	11	22 000	2
1990	1 200 000	120	800 000	80	120 000	12	24 000	2
1995	1 300 000	130	850 000	85	130 000	13	26 000	2
2000	1 400 000	140	900 000	90	140 000	14	28 000	2
2005	1 500 000	150	950 000	95	150 000	15	30 000	3
2010	1 600 000	160	1 000 000	100	160 000	16	32 000	3
2015	1 700 000	170	1 050 000	105	170 000	17	34 000	3
2020	1 800 000	180	1 100 000	110	180 000	18	36 000	3
2025	1 900 000	190	1 150 000	115	190 000	19	38 000	3
2030	2 000 000	200	1 200 000	120	200 000	20	40 000	4
2035	2 100 000	210	1 250 000	125	210 000	21	42 000	4
2040	2 200 000	220	1 300 000	130	220 000	22	44 000	4
2045	2 300 000	230	1 350 000	135	230 000	23	46 000	4
2050	2 400 000	240	1 400 000	140	240 000	24	48 000	4
2055	2 500 000	250	1 450 000	145	250 000	25	50 000	5
2060	2 600 000	260	1 500 000	150	260 000	26	52 000	5
2065	2 700 000	270	1 550 000	155	270 000	27	54 000	5
2070	2 800 000	280	1 600 000	160	280 000	28	56 000	5
2075	2 900 000	290	1 650 000	165	290 000	29	58 000	5
2080	3 000 000	300	1 700 000	170	300 000	30	60 000	6
2085	3 100 000	310	1 750 000	175	310 000	31	62 000	6
2090	3 200 000	320	1 800 000	180	320 000	32	64 000	6
2095	3 300 000	330	1 850 000	185	330 000	33	66 000	6
2100	3 400 000	340	1 900 000	190	340 000	34	68 000	6

<211> 737

<213> Homo Sapien

Met Gln Pro Arg Arg Ala Gln Ala Pro Gly Ala Gln Leu Leu Pro  
1 5 10 15

Ala Leu Ala Leu Leu Leu Leu Leu Gly Ala Gly Pro Arg Gly  
20 25 30

Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro  
35 40 45

Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr  
50 55 60

Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu  
65 70 75

Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn  
80 85 90

Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His  
95 100 105

Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu



110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser	Gly Gly Leu Val Leu Leu	
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly Lys	Cys Thr Thr Lys Pro Ser	
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
395	400	405

Thr Cys Ile Ser	Ser Leu Ser Gly Phe	Thr Cys Gln Cys Pro Glu	410	415	420
Gly Tyr Phe Gly	Ser Ala Cys Glu Glu	Lys Val Asp Pro Cys Ala	425	430	435
Ser Ser Pro Cys	Gln Asn Asn Gly Thr	Cys Tyr Val Asp Gly Val	440	445	450
His Phe Thr Cys	Asn Cys Ser Pro Gly	Phe Thr Gly Pro Thr Cys	455	460	465
Ala Gln Leu Ile	Asp Phe Cys Ala Leu	Ser Pro Cys Ala His Gly	470	475	480
Thr Cys Arg Ser	Val Gly Thr Ser Tyr	Lys Cys Leu Cys Asp Pro	485	490	495
Gly Tyr His Gly	Leu Tyr Cys Glu Glu	Glu Tyr Asn Glu Cys Leu	500	505	510
Ser Ala Pro Cys	Leu Asn Ala Ala Thr	Cys Arg Asp Leu Val Asn	515	520	525
Gly Tyr Glu Cys	Val Cys Leu Ala Glu	Tyr Lys Gly Thr His Cys	530	535	540
Glu Leu Tyr Lys	Asp Pro Cys Ala Asn	Val Ser Cys Leu Asn Gly	545	550	555
Ala Thr Cys Asp	Ser Asp Gly Leu Asn	Gly Thr Cys Ile Cys Ala	560	565	570
Pro Gly Phe Thr	Gly Glu Glu Cys Asp	Ile Asp Ile Asn Glu Cys	575	580	585
Asp Ser Asn Pro	Cys His His Gly Gly	Ser Cys Leu Asp Gln Pro	590	595	600
Asn Gly Tyr Asn	Cys His Cys Pro His	Gly Trp Val Gly Ala Asn	605	610	615
Cys Glu Ile His	Leu Gln Trp Lys Ser	Gly His Met Ala Glu Ser	620	625	630
Leu Thr Asn Met	Pro Arg His Ser Leu	Tyr Ile Ile Ile Gly Ala	635	640	645
Leu Cys Val Ala	Phe Ile Leu Met Leu	Ile Ile Leu Ile Val Gly	650	655	660
Ile Cys Arg Ile	Ser Arg Ile Glu Tyr	Gln Gly Ser Ser Arg Pro	665	670	675
Ala Tyr Glu Glu	Phe Tyr Asn Cys Arg	Ser Ile Asp Ser Glu Phe	680	685	690
Ser Asn Ala Ile	Ala Ser Ile Arg His	Ala Arg Phe Gly Lys Lys			

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp  
 710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys  
 725 730 735

Asp Leu

<210> 16

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 16

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 17

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 18

<211> 508

<212> DNA

<213> Homo Sapien

<400> 18

ctctggaagg tcacggccac aggattccaa cagtgtctccc tcatagatgg 50

acgaaagtgt gacccccctt tcaggctttc aggggggactg gtctctcctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgctg ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19  
<211> 508  
<212> DNA  
<213> Homo Sapien

<400> 19  
ctctggaagg tcacggccac aggattccaa cagtgtctcc tcatagatgg 50  
acgaaagtgt gacccccctt tcaggctttc agggggactg gtcctcctgg 100  
aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150  
tctgtgacta agtctattgt ggctttgctc ttaactctgg tggatgaagg 200  
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250  
gaaaaggaaa atgcaccacg aagccgtcag aggcactttt ttctgtacc 300  
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350  
gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400  
aagatgggag caatttcacc tgtgtttgcc ttctgggta tactggagag 450  
ctttgccaac cgaactgaga ttggagcga cgacctacac cgaactgaga 500  
taggggag 508

<210> 20  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 20  
ctctggaagg tcacggccac agg 23

<210> 21  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
ctcagttcgg ttggcaaagc tctc 24

<210> 22  
<211> 69  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cagtgtctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gctttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

gctgagtctg ctgtctctgc tgctgtgtct ccagcctgta acctgtgcct 50

acaccacgcc agggcccccc agagccctca ccacgctggg cggccccaga 100

gcccacacca tgccggggcac ctacgtctcc tcgaccacac tcagtagtcc 150

cagcaccag ggctgcaag agcaggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgcccc tggctctaag gcagggtttac 250

cagaaagggc tacaggatgt taacctgctc aatttcagct acggccagac 300

cagcctggac aggccttagag atggcctcgt gggcgcccag ttctggtcag 350

cctatgtgcc atgccagacc caggaccggg atgcctgcg cctcaccctg 400

gagcagattg acctcatagc ccgcatgtgt gcctcctatt ctgagctgga 450

gcttgtgacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500

tcacgggtgt agaggggtggc cactcgtctg acaatagcct ctccatctta 550

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gtcagagaca gagtctgact tcaggccagg aactcactga gattcccata 1300  
cactggacag ccaagttacc agccaagtgg tcagtctcag agtcctcccc 1350  
ccacatggcc ccagtccttg cagttgtggc caccttccca gtccttattc 1400  
tgtggctctg atgaccagc tagtctgcc agatgtcact gtagcaagcc 1450  
acagacaccc cacaaagttc ccctgtgtg caggcacaaa tatttctga 1500  
aataaatgtt ttggacatag 1520

<210> 24  
<211> 433  
<212> PRT  
<213> Homo Sapien

<400> 24  
Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser  
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Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe  
20 25 30  
Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln  
35 40 45  
Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser  
50 55 60  
Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly  
65 70 75  
Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg  
80 85 90  
Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg  
95 100 105  
Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys  
110 115 120  
Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu  
125 130 135  
Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe  
140 145 150  
Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn  
155 160 165  
Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr  
170 175 180

Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala	185	190	195
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser	200	205	210
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	215	220	225
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg	230	235	240
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	245	250	255
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro	260	265	270
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys	275	280	285
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp	290	295	300
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	305	310	315
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu	320	325	330
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	335	340	345
Gln	Val	Glu	Lys	Val	Gln	Glu	Glu	Asn	Lys	Trp	Gln	Ser	Pro	Leu	350	355	360
Glu	Asp	Lys	Phe	Pro	Asp	Glu	Gln	Leu	Ser	Ser	Ser	Cys	His	Ser	365	370	375
Asp	Leu	Ser	Arg	Leu	Arg	Gln	Arg	Gln	Ser	Leu	Thr	Ser	Gly	Gln	380	385	390
Glu	Leu	Thr	Glu	Ile	Pro	Ile	His	Trp	Thr	Ala	Lys	Leu	Pro	Ala	395	400	405
Lys	Trp	Ser	Val	Ser	Glu	Ser	Ser	Pro	His	Met	Ala	Pro	Val	Leu	410	415	420
Ala	Val	Val	Ala	Thr	Phe	Pro	Val	Leu	Ile	Leu	Trp	Leu			425	430	

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25  
agttctggtc agcctatgtg cc 22

<210> 26  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
cgtgatggtg tctttgtcca tggg 24

<210> 27  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 27  
ctccaccaat cccgatgaac ttgg 24

<210> 28  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 28  
gagcagattg acctcatagc cgcgatgtgt gcctcctatt ctgagctgga 50

<210> 29  
<211> 1416  
<212> DNA  
<213> Homo Sapien

<400> 29  
aaaacctata aatattccgg attattcata ccgtcccacc atcgggcgcg 50  
gatccgcggc cggaattct aaaccaacat gccgggcacc tacgctccct 100  
cgaccacact cagtagtccc agcaccagg gcctgcaaga gcaggcacgg 150  
gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200  
ggtcctaagg caggtttacc agaaagggt acaggatgtt aacctgcgca 250  
atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300  
ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350  
tgccctgcgc ctcacctgg agcagattga cctcatagc cgcgatgtgtg 400



cctcctattc tgagctggag cttgtgacct cggctaaagc tctgaacgac 450  
 actcagaaat tggcctgcct catcggtgta gagggtggcc actcgctgga 500  
 caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550  
 tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaag 600  
 ggcgtccact ccttctacaa caacatcagc gggctgactg actttggtga 650  
 gaagggtgtg gcagaaatga accgcctggg catgatggta gacttatccc 700  
 atgtctcaga tgctgtggca cggcggggccc tggaagtgtc acaggcacct 750  
 gtgatcttct cccactcggc tgcccgggggt gtgtgcaaca gtgctcggaa 800  
 tgttctgat gacatcctgc agcttctgaa gaagaacggt ggcgtcgtga 850  
 tgggtgtcttt gtccatggga gtaatacagt gcaacccatc agccaatgtg 900  
 tccactgtgg cagatcactt cgaccacatc aaggctgtca ttggatccaa 950  
 gttcatcggg attggtggag attatgatgg ggccggcaaa ttccctcagg 1000  
 ggctggaaga cgtgtccaca taccgggtcc tgatagagga gttgctgagt 1050  
 cgtggctgga gtgaggaaga gcttcagggt gtccttcgtg gaaacctgct 1100  
 gcgggtcttc agacaagtgg aaaaggtaca ggaagaaaac aaatggcaaa 1150  
 gcccttgga ggacaagttc ccggtgagc agctgagcag ttccctgccac 1200  
 tccgacctct cagctctgcg tcagagacag agtctgactt caggccagga 1250  
 actcactgag attcccatc actggacagc caagttacca gccaaagtgt 1300  
 cagtctcaga gtctctcccc caccctgaca aaactcacac atgcccaccg 1350  
 tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc 1400  
 aaaaccaag gacacc 1416

<210> 30  
 <211> 446  
 <212> PRT  
 <213> Homo Sapien

<400> 30  
 Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser  
 1 5 10 15  
 Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe  
 20 25 30  
 Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln  
 35 40 45  
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

				50					55					60
Tyr	Gly	Gln	Thr	Ser 65	Leu	Asp	Arg	Leu	Arg 70	Asp	Gly	Leu	Val	Gly 75
Ala	Gln	Phe	Trp	Ser 80	Ala	Tyr	Val	Pro	Cys 85	Gln	Thr	Gln	Asp	Arg 90
Asp	Ala	Leu	Arg	Leu 95	Thr	Leu	Glu	Gln	Ile 100	Asp	Leu	Ile	Arg	Arg 105
Met	Cys	Ala	Ser	Tyr 110	Ser	Glu	Leu	Glu	Leu 115	Val	Thr	Ser	Ala	Lys 120
Ala	Leu	Asn	Asp	Thr 125	Gln	Lys	Leu	Ala	Cys 130	Leu	Ile	Gly	Val	Glu 135
Gly	Gly	His	Ser	Leu 140	Asp	Asn	Ser	Leu	Ser 145	Ile	Leu	Arg	Thr	Phe 150
Tyr	Met	Leu	Gly	Val 155	Arg	Tyr	Leu	Thr	Leu 160	Thr	His	Thr	Cys	Asn 165
Thr	Pro	Trp	Ala	Glu 170	Ser	Ser	Ala	Lys	Gly 175	Val	His	Ser	Phe	Tyr 180
Asn	Asn	Ile	Ser	Gly 185	Leu	Thr	Asp	Phe	Gly 190	Glu	Lys	Val	Val	Ala 195
Glu	Met	Asn	Arg	Leu 200	Gly	Met	Met	Val	Asp 205	Leu	Ser	His	Val	Ser 210
Asp	Ala	Val	Ala	Arg 215	Arg	Ala	Leu	Glu	Val 220	Ser	Gln	Ala	Pro	Val 225
Ile	Phe	Ser	His	Ser 230	Ala	Ala	Arg	Gly	Val 235	Cys	Asn	Ser	Ala	Arg 240
Asn	Val	Pro	Asp	Asp 245	Ile	Leu	Gln	Leu	Leu 250	Lys	Lys	Asn	Gly	Gly 255
Val	Val	Met	Val	Ser 260	Leu	Ser	Met	Gly	Val 265	Ile	Gln	Cys	Asn	Pro 270
Ser	Ala	Asn	Val	Ser 275	Thr	Val	Ala	Asp	His 280	Phe	Asp	His	Ile	Lys 285
Ala	Val	Ile	Gly	Ser 290	Lys	Phe	Ile	Gly	Ile 295	Gly	Gly	Asp	Tyr	Asp 300
Gly	Ala	Gly	Lys	Phe 305	Pro	Gln	Gly	Leu	Glu 310	Asp	Val	Ser	Thr	Tyr 315
Pro	Val	Leu	Ile	Glu 320	Glu	Leu	Leu	Ser	Arg 325	Gly	Trp	Ser	Glu	Glu 330
Glu	Leu	Gln	Gly	Val 335	Leu	Arg	Gly	Asn	Leu 340	Leu	Arg	Val	Phe	Arg 345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu	350	355	360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser	365	370	375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln	380	385	390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala	395	400	405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His	410	415	420
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser	425	430	435
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	440	445	

<210> 31  
 <211> 1790  
 <212> DNA  
 <213> Homo Sapien

<400> 31  
 cgcccagcga cgtgcggggcg gectggcccg cgccctcccg cgcccggcct 50  
 gcgctcccgcg cctgcgcca ccgcgcgcca gccgcagccc gccgcgcgcc 100  
 ccgggcagcg ccggcccccatt gccgcgcggc cgccggggcc ccgcgcgcca 150  
 atccgcgcgg cgccgcgcgc cgttgctgcc cctgctgctg ctgctctgcg 200  
 tccctggggc gccgcgagcc ggatcaggag cccacacagc tgtgatcagt 250  
 ccccaggatc ccacgcttct catcggtctc tccctgctgg ccacctgctc 300  
 agtgcaaggga gaccaccag gaggccgcgc cgaggggctc tactggacct 350  
 tcaacggggc cgccctgccc cctgagctct cccgtgtact caacgcctcc 400  
 accttggtc tggccctggc caacctcaat ggggtccaggc agcggtcggg 450  
 ggacaacctc gtgtgccacg cccgtgacgg cagcatcctg gctggctcct 500  
 gctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550  
 tccaagaaca tgaaggactt gacctgccgc tggacgccag gggcccacgg 600  
 ggagaccttc ctccacacca actactccct caagtacaag cttaggtggg 650  
 atggccagga caacacatgt gaggagtacc acacagtggg gcccactcc 700  
 tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750  
 ggaggccacc aaccgctgg gctctgcccg ctccgatgta ctcacgctgg 800

**SECRET**

<211> 422

<213> Homo Sapien

Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg  
1 5 10 15

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro  
35 40 45

28

Ser Val His Gly Asp	Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr	65	70	75
Trp Thr Leu Asn Gly Arg Arg Leu Pro	Pro Glu Leu Ser Arg Val	80	85	90
Leu Asn Ala Ser Thr Leu Ala Leu Ala	Leu Ala Asn Leu Asn Gly	95	100	105
Ser Arg Gln Arg Ser Gly Asp Asn Leu	Val Cys His Ala Arg Asp	110	115	120
Gly Ser Ile Leu Ala Gly Ser Cys Leu	Tyr Val Gly Leu Pro Pro	125	130	135
Glu Lys Pro Val Asn Ile Ser Cys Trp	Ser Lys Asn Met Lys Asp	140	145	150
Leu Thr Cys Arg Trp Thr Pro Gly Ala	His Gly Glu Thr Phe Leu	155	160	165
His Thr Asn Tyr Ser Leu Lys Tyr Lys	Leu Arg Trp Tyr Gly Gln	170	175	180
Asp Asn Thr Cys Glu Glu Tyr His Thr	Val Gly Pro His Ser Cys	185	190	195
His Ile Pro Lys Asp Leu Ala Leu Phe	Thr Pro Tyr Glu Ile Trp	200	205	210
Val Glu Ala Thr Asn Arg Leu Gly Ser	Ala Arg Ser Asp Val Leu	215	220	225
Thr Leu Asp Ile Leu Asp Val Val Thr	Thr Asp Pro Pro Pro Asp	230	235	240
Val His Val Ser Arg Val Gly Gly Leu	Glu Asp Gln Leu Ser Val	245	250	255
Arg Trp Val Ser Pro Pro Ala Leu Lys	Asp Phe Leu Phe Gln Ala	260	265	270
Lys Tyr Gln Ile Arg Tyr Arg Val Glu	Asp Ser Val Asp Trp Lys	275	280	285
Val Val Asp Asp Val Ser Asn Gln Thr	Ser Cys Arg Leu Ala Gly	290	295	300
Leu Lys Pro Gly Thr Val Tyr Phe Val	Gln Val Arg Cys Asn Pro	305	310	315
Phe Gly Ile Tyr Gly Ser Lys Lys Ala	Gly Ile Trp Ser Glu Trp	320	325	330
Ser His Pro Thr Ala Ala Ser Thr Pro	Arg Ser Glu Arg Pro Gly	335	340	345
Pro Gly Gly Gly Ala Cys Glu Pro Arg	Gly Gly Glu Pro Ser Ser			

TOP SECRET

350	355	360
Gly Pro Val Arg Arg Glu Leu Lys Gln	Phe Leu Gly Trp Leu Lys	
365	370	375
Lys His Ala Tyr Cys Ser Asn Leu Ser	Phe Arg Leu Tyr Asp Gln	
380	385	390
Trp Arg Ala Trp Met Gln Lys Ser His	Lys Thr Arg Asn Gln Asp	
395	400	405
Glu Gly Ile Leu Pro Ser Gly Arg Arg	Gly Thr Ala Arg Gly Pro	
410	415	420
Ala Arg		

<210> 33  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
cccgcccgac gtgcacgtga gcc 23

<210> 34  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 34  
tgagccagcc caggaactgc ttg 23

<210> 35  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 35  
caagtgcgct gcaaccctt tggcatctat ggctccaaga aagccgggat 50

<210> 36  
<211> 1771  
<212> DNA  
<213> Homo Sapien

<400> 36  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacaccaaaa cgctcgcagc cacaaaaggg 100  
 atgaaatttc ttctggacat cctcctgctt ctcccgttac tgatcgtctg 150  
 ctccctagag tccttcgtga agctttttat tcctaagagg agaaaatcag 200  
 tcaccggcga aatcgtgctg attacaggag ctgggcatgg aattgggaga 250  
 ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
 tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350  
 gtgccaaggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400  
 tacagctctg caaagaaggt gaaggcagaa attggagatg ttagtatttt 450  
 agtaaataat gctggtgtag tctatacatc agatttgttt gctacacaag 500  
 atcctcagat tgaaaagact tttgaagtta atgtacttgc acatttctgg 550  
 actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600  
 tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg 650  
 cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 700  
 gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg 750  
 tcctaatttc gtaaacactg gcttcatcaa aaatccaagt acaagtttgg 800  
 gaccactctt ggaacctgag gaagtggtaa acaggctgat gcacgggatt 850  
 ctgactgagc agaagatgat ttttattcca tcttctatag cttttttaac 900  
 aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa 950  
 aaatcagtgat taagtttgat gcagttattg gatataaaat gaaagcgcaa 1000  
 taagcaccta gttttctgaa aactgattta ccaggtttag gttgatgtca 1050  
 tctaatagtg ccagaatttt aatgtttgaa cttctgtttt ttctaattat 1100  
 cccattttct tcaatatcat ttttgaggct ttggcagtct tcatttacta 1150  
 ccacttggtc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
 tacctttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac 1250  
 tttattaaaa taatttccaa gattatttgt ggctcacctg aaggctttgc 1300  
 aaaatttgta ccataaccgt ttatttaaca tatattttta tttttgattg 1350  
 cacttaaaatt ttgtataatt tgtgtttctt tttctgttct acataaaatc 1400  
 agaaacttca agctctctaa ataaaatgaa ggactatata tagtggtatt 1450  
 tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctacccatt 1500

[illegible]

<400> 37

32



TOP SECRET 42344650

200	205	210
Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe		
215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 38  
ggtgaaggca gaaattggag atg 23

<210> 39  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
atcccatgca tcagcctgtt tacc 24

<210> 40  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 40  
gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 41  
<211> 1377  
<212> DNA  
<213> Homo Sapien



<400> 41

gactagttct cttggagtct gggaggagga aagcggagcc ggcagggagc 50  
gaaccaggac tggggtgacg gcagggcagg gggcgccctgg ccggggagaa 100  
gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150  
ccgaaggagg ccatcgggga gccgggaggg gggactgcga gaggaccccg 200  
gcgtccgggc tcccggtgcc agcgctatga ggccactcct cgtcctgctg 250  
ctcctggggc tggcgcccg ctcgccccca ctggacgaca acaagatccc 300  
cagcctctgc ccggggcacc ccggccttcc aggcacgccg ggccaccatg 350  
gcagccaggg cttgccgggc cgcgatggcc gcgacggccg cgacggcgcg 400  
cccggggctc cgggagagaa aggcgagggc gggaggccgg gactgccggg 450  
acctcgaggg gaccccgggc cgcgaggaga ggcgggaccc gcggggccca 500  
ccgggcctgc cggggagtgc tcggtgcctc cgcgatccgc cttcagcgcc 550  
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cgaccgcgtg ctggtgaacg agcagggaca ttacgacgcc gtcaccggca 650  
agttcacctg ccagggtgect ggggtctact acttcgccgt ccatgccacc 700  
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tgectcttct ttccagtttt tcgggggggtg gccaagcca gcctcgctct 800  
cggggggggc catggtgagg ctggagcctg aggaccaagt gtgggtgcag 850  
gtgggtgtgg gtgactacat tggcatctat gccagcatca agacagacag 900  
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gggtgtgagg ctgacaacca ggtcatccag gagggtggc ccccctggaa 1050  
tattgtgaat gactagggag gtggggtaga gcaactctcg tcctgctgct 1100  
ggcaaggaat gggaacagtg gctgtctgcg atcaggtctg gcagcatggg 1150  
gcagtggctg gatttctgcc caagaccaga ggagtgtgct gtgctggcaa 1200  
gtgtaagtcc ccagttgct ctggtccagg agcccacggg ggggtgctct 1250  
cttctgggc ctctgcttct ctggatcctc cccacccct cctgctcctg 1300  
gggcggggc ttttctcaga gatcactcaa taaacctaag aaccctcata 1350  
aaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243  
 <212> PRT  
 <213> Homo Sapien

<400> 42

Met	Arg	Pro	Leu	Leu	Val	Leu	Leu	Leu	Leu	Gly	Leu	Ala	Ala	Gly	1	5	10	15
Ser	Pro	Pro	Leu	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	20	25	30		
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43  
 <211> 24

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 43  
   tacaggccca gtcaggacca gggg 24  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 44  
   agccagcctc gctctcgg 18  
  
 <210> 45  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 45  
   gtctgcatc aggtctgg 18  
  
 <210> 46  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 46  
   gaaagaggca atggattcgc 20  
  
 <210> 47  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 47  
   gacttacact tgccagcaca gcac 24  
  
 <210> 48  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gctgactcc tggagattgt gaatagctcc 50  
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100  
acctgacggg cccaacagac ccatgctgca tccagagacc tcccctggcc 150  
gggggcatct cctggctgtg ctectggccc tccttggcac cacctgggca 200  
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cccgagcctg gcacccggcc tgtggcgcac cctgcaagtg ggctggaaca 450  
tgcagctgct gcccggggc ttggcgctct ttgttgaagt ggtcagccta 500  
tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550  
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gacaatcatc cctataaga agggcgctg gtgttcgctc tgcacagcca 750  
gtgtctcagg ctgcttcaaa gctgggacc atgcaggggg gctctgtgag 800  
gtccccagga atccttgtcg catgagctgc cagaaccatg gacgtctcaa 850  
catcagcacc tgcaactgcc actgtccccc tggctacacg ggcagatact 900  
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gagtgtctcg gcgtctgtga catcggttac gggggagccc agtgtgccac 1000  
caaggtgcat ttcccttcc acacctgtga cctgaggatc gacggagact 1050  
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 cagttttgcc tttgggcagc ctgacaacca cgggctggtg tggctgagtg 1350  
 ctgccatggg gtttggcaac tgcgtggagc tgcaggcttc agctgccttc 1400  
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 catggtcccc tcgctgccc tgggagcacc ggctctgctt acctgtctgc 1550  
 ccacctgtct ggaacaaggg ccaggttaag accacatgcc tcatgtccaa 1600  
 agaggtctca gaccttgac aatgccagaa gttgggcaga gagaggcagg 1650  
 gaggccagtg agggccaggg agtgagtgtt agaagaagct ggggcccttc 1700  
 gcctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750  
 acaccgccag tggtcacaaa aggctgctct cttccacctg gccagaccc 1800  
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 tatgaatcag ctgaaaaaaaa aaaaaa 1876

<210> 50

<211> 455

<212> PRT

<213> Homo Sapien

<400> 50

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Val	Leu	Leu	Ala	Leu	Leu	Gly	Thr	Thr	Trp	Ala	Glu	Val	Trp	Pro
				20					25					30

Pro	Gln	Leu	Gln	Glu	Gln	Ala	Pro	Met	Ala	Gly	Ala	Leu	Asn	Arg
				35					40					45

Lys	Glu	Ser	Phe	Leu	Leu	Leu	Ser	Leu	His	Asn	Arg	Leu	Arg	Ser
				50					55					60

Trp	Val	Gln	Pro	Pro	Ala	Ala	Asp	Met	Arg	Arg	Leu	Asp	Trp	Ser
				65					70					75

Asp	Ser	Leu	Ala	Gln	Leu	Ala	Gln	Ala	Arg	Ala	Ala	Leu	Cys	Gly
				80					85					90

Ile	Pro	Thr	Pro	Ser	Leu	Ala	Ser	Gly	Leu	Trp	Arg	Thr	Leu	Gln
				95					100					105

Val	Gly	Trp	Asn	Met	Gln	Leu	Leu	Pro	Ala	Gly	Leu	Ala	Ser	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

110										115					120				
Val	Glu	Val	Val	Ser	Leu	Trp	Phe	Ala	Glu	Gly	Gln	Arg	Tyr	Ser					
				125					130					135					
His	Ala	Ala	Gly	Glu	Cys	Ala	Arg	Asn	Ala	Thr	Cys	Thr	His	Tyr					
				140					145					150					
Thr	Gln	Leu	Val	Trp	Ala	Thr	Ser	Ser	Gln	Leu	Gly	Cys	Gly	Arg					
				155					160					165					
His	Leu	Cys	Ser	Ala	Gly	Gln	Thr	Ala	Ile	Glu	Ala	Phe	Val	Cys					
				170					175					180					
Ala	Tyr	Ser	Pro	Gly	Gly	Asn	Trp	Glu	Val	Asn	Gly	Lys	Thr	Ile					
				185					190					195					
Ile	Pro	Tyr	Lys	Lys	Gly	Ala	Trp	Cys	Ser	Leu	Cys	Thr	Ala	Ser					
				200					205					210					
Val	Ser	Gly	Cys	Phe	Lys	Ala	Trp	Asp	His	Ala	Gly	Gly	Leu	Cys					
				215					220					225					
Glu	Val	Pro	Arg	Asn	Pro	Cys	Arg	Met	Ser	Cys	Gln	Asn	His	Gly					
				230					235					240					
Arg	Leu	Asn	Ile	Ser	Thr	Cys	His	Cys	His	Cys	Pro	Pro	Gly	Tyr					
				245					250					255					
Thr	Gly	Arg	Tyr	Cys	Gln	Val	Arg	Cys	Ser	Leu	Gln	Cys	Val	His					
				260					265					270					
Gly	Arg	Phe	Arg	Glu	Glu	Glu	Cys	Ser	Cys	Val	Cys	Asp	Ile	Gly					
				275					280					285					
Tyr	Gly	Gly	Ala	Gln	Cys	Ala	Thr	Lys	Val	His	Phe	Pro	Phe	His					
				290					295					300					
Thr	Cys	Asp	Leu	Arg	Ile	Asp	Gly	Asp	Cys	Phe	Met	Val	Ser	Ser					
				305					310					315					
Glu	Ala	Asp	Thr	Tyr	Tyr	Arg	Ala	Arg	Met	Lys	Cys	Gln	Arg	Lys					
				320					325					330					
Gly	Gly	Val	Leu	Ala	Gln	Ile	Lys	Ser	Gln	Lys	Val	Gln	Asp	Ile					
				335					340					345					
Leu	Ala	Phe	Tyr	Leu	Gly	Arg	Leu	Glu	Thr	Thr	Asn	Glu	Val	Thr					
				350					355					360					
Asp	Ser	Asp	Phe	Glu	Thr	Arg	Asn	Phe	Trp	Ile	Gly	Leu	Thr	Tyr					
				365					370					375					
Lys	Thr	Ala	Lys	Asp	Ser	Phe	Arg	Trp	Ala	Thr	Gly	Glu	His	Gln					
				380					385					390					
Ala	Phe	Thr	Ser	Phe	Ala	Phe	Gly	Gln	Pro	Asp	Asn	His	Gly	Leu					
				395					400					405					

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu  
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr  
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg  
440 445 450

Trp Gly Pro Gly Ser  
455

<210> 51  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 51  
aggaacttct ggatcgggct cacc 24

<210> 52  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 52  
gggtctgggc caggtggaag agag 24

<210> 53  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 53  
gccaaggact ccttccgctg ggccacaggg gagcaccagg ccttc 45

<210> 54  
<211> 2331  
<212> DNA  
<213> Homo Sapien

<400> 54  
cggacgcgtg ggctgggcgc tgcaaagcgt gtcccgcggt gtccccgagc 50  
gtcccgcgcc ctgcctccgc catgctcctg ctgctggggc tgtgcctggg 100  
gctgtccctg tgtgtggggt cgcaggaaga ggcgcagagc tggggccact 150  
cttcggagca ggatggactc aggggtcccga ggcaagtcag actgttgcag 200



aggctgaaaa ccaaaccctt gatgacagaa ttctcagtga agtctacat 250  
catttcccggt tatgccttca ctacgggttc ctgcagaatg ctgaacagag 300  
cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350  
ttcatcacca acttcactat gcttattgga gacaagggtgt atcagggcga 400  
aattacagag agagaaaaga agagtgggtga tagggtaaaa gagaaaagga 450  
ataaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500  
tctgcagtga ttcccagcaa ggacaaagcc gcctttttcc tgagttatga 550  
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gaggggcagt gggcgcgggg aagatgattc tgggcctccc ccatctactg 750  
tcattaacca aaatgaaaca ttgccaaca taatttttaa acctactgta 800  
gtacaacaag ccaggattgc ccagaatgga attttgggag actttatcat 850  
tagatatgac gtcaatagag aacagagcat tggggacatc caggttctaa 900  
atggctatct tgtgcactac ttgtctcta aagaccttc tctttaccc 950  
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cccaggaccg ttctcagtac attggatttt ccaaccggat caaagtatgg 1100  
aaggaccact tgatatcagt cactccagac agcatcaggg atgggaaagt 1150  
gtacattcac catatgtcac ccactggagg cacagacatc aacggggccc 1200  
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ggagaccgga gcgtgtccct catcgtcttc ctgacggatg ggaagcccac 1300  
ggtcggggag acgcacaccc tcaagatcct caacaacacc cgagaggccg 1350  
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cgtgcacgag gaggaggacg caggctcgca gctcatcggg ttctacgatg 1500  
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tcagtgggtg aggccaccaa gacctgttc cccaactact tcaacggctc 1600  
ggagatcatc attgcgggga agctgggtgga caggaagctg gatcacctgc 1650

姓名	性别	年龄	籍贯	职业	文化程度	健康状况	婚姻状况	子女情况	其他
王德胜	男	45	山东	工人	高中	良好	已婚	2子1女	
李秀英	女	38	河北	教师	大学	良好	已婚	1子1女	
张国强	男	52	河南	农民	初中	一般	已婚	3子2女	
赵红梅	女	41	江苏	医生	大专	良好	已婚	1子1女	
刘伟明	男	35	浙江	工程师	本科	良好	已婚	1子1女	
陈丽娟	女	48	安徽	护士	中专	良好	已婚	2子1女	
周建民	男	55	湖北	干部	高中	一般	已婚	3子2女	
吴晓芳	女	32	四川	会计	大专	良好	已婚	1子1女	
孙志远	男	43	湖南	工人	初中	一般	已婚	2子1女	
郑雅婷	女	39	广东	教师	大学	良好	已婚	1子1女	
冯志强	男	50	广西	农民	小学	一般	已婚	3子2女	
马静雯	女	44	福建	医生	本科	良好	已婚	1子1女	
徐文博	男	37	江西	工程师	大专	良好	已婚	1子1女	
黄丽娟	女	46	山西	护士	中专	良好	已婚	2子1女	
周建民	男	55	湖北	干部	高中	一般	已婚	3子2女	
吴晓芳	女	32	四川	会计	大专	良好	已婚	1子1女	
孙志远	男	43	湖南	工人	初中	一般	已婚	2子1女	
郑雅婷	女	39	广东	教师	大学	良好	已婚	1子1女	
冯志强	男	50	广西	农民	小学	一般	已婚	3子2女	
马静雯	女	44	福建	医生	本科	良好	已婚	1子1女	
徐文博	男	37	江西	工程师	大专	良好	已婚	1子1女	
黄丽娟	女	46	山西	护士	中专	良好	已婚	2子1女	

<211> 694

<213> Homo Sapien

Met Leu Leu Leu Leu Gly Leu Cys Leu Gly Leu Ser Leu Cys Val  
1 5 10 15

Gly Ser Gln Glu Glu Ala Gln Ser Trp Gly His Ser Ser Glu Gln  
20 25 30

Asp Gly Leu Arg Val Pro Arg Gln Val Arg Leu Leu Gln Arg Leu  
35 40 45

Lys Thr Lys Pro Leu Met Thr Glu Phe Ser Val Lys Ser Thr Ile  
50 55 60

Ile Ser Arg Tyr Ala Phe Thr Thr Val Ser Cys Arg Met Leu Asn  
65 70 75

Arg Ala Ser Glu Asp Gln Asp Ile Glu Phe Gln Met Gln Ile Pro  
80 85 90

Ala Ala Ala Phe Ile Thr Asn Phe Thr Met Leu Ile Gly Asp Lys  
95 100 105

Val Tyr Gln Gly Glu Ile Thr Glu Arg Glu Lys Lys Ser Gly Asp  
110 115 120

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu			

410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr		
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu		
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu		
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr		
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val		
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser		
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His		
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile		
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp		
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr		
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu		
575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg		
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu		
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met		
620	625	630
Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro		
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly		
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys		
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His		
680	685	690
Leu Gly Ile Arg		

<210> 56  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 56  
gtgggaacca aactccggca gacc 24

<210> 57  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 57  
cacatcgagc gtctctgg 18

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 58  
agccgctcct tctccggttc atcg 24

<210> 59  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 59  
tggaaggacc acttgatc agtcactcca gacagcatca gggatggg 48

<210> 60  
<211> 1413  
<212> DNA  
<213> Homo Sapien

<400> 60  
cggacgcgtg ggggtgcccga catggcgagt gtagtgctgc cgagcggatc 50  
ccagtgtgcg gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100  
tgctgttgct cttctccgcc gcggcactga tccccacagg tgatgggcag 150  
aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgaccat 200

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250  
ccaacaggca gaccatttat ttcagggaact tcaggccttt gaaggacagc 300  
aggtttcagt tgctgaattt ttctagcagt gaactcaaag tatcattgac 350  
aaacgtctca atttctgatg aaggaagata cttttgccag ctctataaccg 400  
atccccaca ggaaagttac accaccatca cagtcctggt cccaccacgt 450  
aatctgatga tcgatatcca gaaagacact gcggtggaag gtgaggagat 500  
tgaagtcaac tgactgcta tggccagcaa gccagccacg actatcaggt 550  
ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600  
tcagacatgt aactgtgac cagtcagctg atgctgaagg tgcacaagga 650  
ggacgatggg gtcccagtga tctgccaggt ggagcaccct gcggtcactg 700  
gaaacctgca gaccagcgg tatctagaag tacagtataa gcctcaagtg 750  
cacattcaga tgacttatcc tctacaaggc ttaaccggg aaggggacgc 800  
gcttgagtta acatgtgaag ccatcgggaa gcccagcct gtgatggtaa 850  
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cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataaccg 950  
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accaccacca ccaccaccac caccatcctt accatcatca cagattcccg 1100  
agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcggtg 1150  
gcgtcggtggc ggtggtggtg ttcgccatgc tgtgcttgct catcattctg 1200  
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gaggacagaa caactccgaa gaaaagaaag agtacttcat ctagatcagc 1350  
ctttttgttt caatgaggtg tccaactggc cctattttaga tgataaagag 1400  
acagtgatat tgg 1413

<210> 61  
<211> 440  
<212> PRT  
<213> Homo Sapien

<400> 61  
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala  
1 5 10 15

Ala Ala Ala Ala	Ala Pro Pro Gly Leu Arg Leu Leu Leu Leu Leu	20	25	30
Phe Ser Ala Ala	Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu	35	40	45
Phe Thr Lys Asp	Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile	50	55	60
Ser Cys Gln Val	Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu	65	70	75
Asn Pro Asn Arg	Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu	80	85	90
Lys Asp Ser Arg	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu	95	100	105
Lys Val Ser Leu	Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr	110	115	120
Phe Cys Gln Leu	Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr	125	130	135
Ile Thr Val Leu	Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln	140	145	150
Lys Asp Thr Ala	Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr	155	160	165
Ala Met Ala Ser	Lys Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly	170	175	180
Asn Thr Glu Leu	Lys Gly Lys Ser Glu Val Glu Glu Trp Ser Asp	185	190	195
Met Tyr Thr Val	Thr Ser Gln Leu Met Leu Lys Val His Lys Glu	200	205	210
Asp Asp Gly Val	Pro Val Ile Cys Gln Val Glu His Pro Ala Val	215	220	225
Thr Gly Asn Leu	Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys	230	235	240
Pro Gln Val His	Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr	245	250	255
Arg Glu Gly Asp	Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys	260	265	270
Pro Gln Pro Val	Met Val Thr Trp Val Arg Val Asp Asp Glu Met	275	280	285
Pro Gln His Ala	Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn	290	295	300
Leu Asn Lys Thr	Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn			



305

310

315

Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp  
320 325 330

Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr  
335 340 345

Thr Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg  
350 355 360

Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile  
365 370 375

Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu  
380 385 390

Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe  
395 400 405

Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr  
410 415 420

Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys  
425 430 435

Lys Glu Tyr Phe Ile  
440

&lt;210&gt; 62

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 62

ggcttctgct gttgctcttc tccg 24

&lt;210&gt; 63

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 63

gtacactgtg accagtcagc 20

&lt;210&gt; 64

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe



<400> 64  
atcatcacag attcccgagc 20

<210> 65  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
ttcaatctcc tcaccttcca ccgc 24

<210> 66  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 66  
atagctgtgt ctgcgtctgc tgcg 24

<210> 67  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 67  
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68  
<211> 2555  
<212> DNA  
<213> Homo Sapien

<400> 68  
ggggcggtg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50  
cctcggggcc gaccgccag gaaagactga ggccgcggcc tgccccgcc 100  
ggctccctgc gccgccgcc cctcccgga cagaagatgt gctccagggt 150  
ccctctgctg ctgccgctgc tcctgtact ggccctgggg cctgggggtgc 200  
agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250  
actgcccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggt 300  
ggggctgtac gtctttgaga acggcatcac catgctcgac gcaagcagct 350  
ttgccggcct gccgggcctg cagctcctgg acctgtcaca gaaccagatc 400



05944334-033101

gcgggtctga gtgtgaggtg ccactcatgg gcttcccagg gcctggcctc 1900  
cagtcacccc tccacgcaaa gccctacatc taagccagag agagacaggg 1950  
cagctggggc cgggctctca gccagtgaga tggccagccc cctcctgctg 2000  
ccacaccacg taagttctca gtcccaacct cggggatgtg tgcagacagg 2050  
gctgtgtgac cacagctggg ccctgttccc tctggacctc ggtctcctca 2100  
tctgtgagat gctgtggccc agctgacgag ccctaacgtc ccagaaccg 2150  
agtgcctatg aggacagtgt ccgccctgcc ctccgcaacg tgcagtcctt 2200  
gggcacggcg ggccctgcc tgtgctggta acgcatgcct gggccctgct 2250  
gggctctccc actccaggcg gaccctgggg gccagtgaag gaagctcccg 2300  
gaaagagcag agggagagcg ggtaggcggc tgtgtgactc tagtcttggc 2350  
cccaggaagc gaaggaacaa aagaaactgg aaaggaagat gctttaggaa 2400  
catgttttgc ttttttaaaa tatatatata tttataagag atcctttccc 2450  
atttattctg ggaagatgtt tttcaaactc agagacaagg actttggttt 2500  
ttgtaagaca aacgatgata tgaaggcctt ttgtaagaaa aaataaaaaa 2550  
aaaaa 2555

<210> 69  
<211> 598  
<212> PRT  
<213> Homo Sapien

<400> 69  
Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu  
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Ala Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys  
20 25 30  
Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr  
35 40 45  
Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe  
50 55 60  
Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu  
65 70 75  
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95 100 105  
Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

				110					115					120
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Leu	Phe	Ser	Arg	Leu 140	Arg	Asn	Leu	His	Asp 145	Leu	Asp	Val	Ser	Asp 150
Asn	Gln	Leu	Glu	Arg 155	Val	Pro	Pro	Val	Ile 160	Arg	Gly	Leu	Arg	Gly 165
Leu	Thr	Arg	Leu	Arg 170	Leu	Ala	Gly	Asn	Thr 175	Arg	Ile	Ala	Gln	Leu 180
Arg	Pro	Glu	Asp	Leu 185	Ala	Gly	Leu	Ala	Ala 190	Leu	Gln	Glu	Leu	Asp 195
Val	Ser	Asn	Leu	Ser 200	Leu	Gln	Ala	Leu	Pro 205	Gly	Asp	Leu	Ser	Gly 210
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Ser	His	Val	Thr	Leu 245	Ala	Ser	Pro	Glu	Glu 250	Thr	Arg	Cys	His	Phe 255
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Thr	Arg	Pro	Val	Val 290	Arg	Glu	Pro	Thr	Ala 295	Leu	Ser	Ser	Ser	Leu 300
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Ser	Pro	Pro	Ser	Thr 320	Ala	Pro	Pro	Thr	Val 325	Gly	Pro	Val	Pro	Gln 330
Pro	Gln	Asp	Cys	Pro 335	Pro	Ser	Thr	Cys	Leu 340	Asn	Gly	Gly	Thr	Cys 345
His	Leu	Gly	Thr	Arg 350	His	His	Leu	Ala	Cys 355	Leu	Cys	Pro	Glu	Gly 360
Phe	Thr	Gly	Leu	Tyr 365	Cys	Glu	Ser	Gln	Met 370	Gly	Gln	Gly	Thr	Arg 375
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[illegible]

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<223> Synthetic oligonucleotide probe

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<211> 24

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<223> Synthetic oligonucleotide probe

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[illegible]

<213> Homo Sapien

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Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	Arg	Gly	Arg	Gly	Leu	Gln	Ala
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Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	Ala	Gly	Val	Tyr	Leu	Leu
				155					160					165
Tyr	Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	Phe	Thr	Met	Gly	Gln
				170					175					180
Val	Val	Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	Thr	Leu	Phe	Arg
				185					190					195
Cys	Ile	Arg	Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser
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Cys	Tyr	Ser	Ala	Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu
				215					220					225
Ser	Val	Ile	Ile	Pro	Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro
				230					235					240
His	Gly	Thr	Phe	Leu	Gly	Phe	Val	Lys	Leu					
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<211> 2849

<212> DNA

<213> Homo Sapien

<400> 77

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<211> 281

<212> PRT

<213> Homo Sapien

<400> 78

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Gln	Gly	Glu	Gln	Gln	Glu	Trp	Glu	Gly	Thr	Glu	Glu	Leu	Pro	Ser
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Pro	Pro	Asp	His	Ala	Glu	Arg	Ala	Glu	Glu	Gln	His	Glu	Lys	Tyr
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Arg	Pro	Ser	Gln	Asp	Gln	Gly	Leu	Pro	Ala	Ser	Arg	Cys	Leu	Arg
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Cys	Cys	Asp	Pro	Gly	Thr	Ser	Met	Tyr	Pro	Ala	Thr	Ala	Val	Pro
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Gln	Ile	Asn	Ile	Thr	Ile	Leu	Lys	Gly	Glu	Lys	Gly	Asp	Arg	Gly
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Asp	Arg	Gly	Leu	Gln	Gly	Lys	Tyr	Gly	Lys	Thr	Gly	Ser	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
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<210> 81

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10

15

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Lys Lys Ser Leu Glu	Asp Val Val Ile	Asp Ile Gln Ser Ser Leu	35	40	45
Ser Lys Gly Ile Arg	Gly Asn Glu Pro	Val Tyr Thr Ser Thr Gln	50	55	60
Glu Asp Cys Ile Asn	Ser Cys Cys Ser	Thr Lys Asn Ile Ser Gly	65	70	75
Asp Lys Ala Cys Asn	Leu Met Ile Phe	Asp Thr Arg Lys Thr Ala	80	85	90
Arg Gln Pro Asn Cys	Tyr Leu Phe Phe	Cys Pro Asn Glu Glu Ala	95	100	105
Cys Pro Leu Lys Pro	Ala Lys Gly Leu	Met Ser Tyr Arg Ile Ile	110	115	120
Thr Asp Phe Pro Ser	Leu Thr Arg Asn	Leu Pro Ser Gln Glu Leu	125	130	135
Pro Gln Glu Asp Ser	Leu Leu His Gly	Gln Phe Ser Gln Ala Val	140	145	150
Thr Pro Leu Ala His	His His Thr Asp	Tyr Ser Lys Pro Thr Asp	155	160	165
Ile Ser Trp Arg Asp	Thr Leu Ser Gln	Lys Phe Gly Ser Ser Asp	170	175	180
His Leu Glu Lys Leu	Phe Lys Met Asp	Glu Ala Ser Ala Gln Leu	185	190	195
Leu Ala Tyr Lys Glu	Lys Gly His Ser	Gln Ser Ser Gln Phe Ser	200	205	210
Ser Asp Gln Glu Ile	Ala His Leu Leu	Pro Glu Asn Val Ser Ala	215	220	225
Leu Pro Ala Thr Val	Ala Val Ala Ser	Pro His Thr Thr Ser Ala	230	235	240
Thr Pro Lys Pro Ala	Thr Leu Leu Pro	Thr Asn Ala Ser Val Thr	245	250	255
Pro Ser Gly Thr Ser	Gln Pro Gln Leu	Ala Thr Thr Ala Pro Pro	260	265	270
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Val Phe Thr Arg Ala	Ala Ala Thr Leu	Gln Ala Met Ala Thr Thr	290	295	300
Ala Val Leu Thr Thr	Thr Phe Gln Ala	Pro Thr Asp Ser Lys Gly			

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 Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg  
 50 55 60  
 Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala  
 65 70 75  
 Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile  
 80 85 90  
 Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val  
 95 100 105  
 Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn  
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 Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser  
 125 130 135  
 Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu  
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Asn	Met	Lys	Phe	Arg	Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly
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Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser
			200						205					210
Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln
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